WHAT IS CLAIMED:

1. A method of conducting a reduced dimensionality three-dimensional (3D) HA,CA,(CO),N,HN nuclear magnetic resonance (NMR) experiment by measuring the chemical shift values for the following nuclei of a protein molecule having two consecutive amino acid residues, *i*-1 and *i*: (1) an α-proton of amino acid residue *i*-1, $^{1}H^{\alpha}_{i-1}$; (2) an α-carbon of amino acid residue *i*-1, $^{13}C^{\alpha}_{i-1}$; (3) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, said method comprising:

providing a protein sample;

applying radiofrequency pulses to the protein sample which effect a nuclear spin polarization transfer wherein the chemical shift evolutions of $^{1}H^{\alpha}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ of amino acid residue *i*-1 are connected to the chemical shift evolutions of $^{15}N_i$ and $^{1}H^{N}_{i}$ of amino acid residue *i*, under conditions effective (1) to generate NMR signals encoding the chemical shift values of $^{13}C^{\alpha}_{i-1}$ and $^{15}N_i$ in a phase sensitive manner in two indirect time domain dimensions, $t_1(^{13}C^{\alpha})$ and $t_2(^{15}N)$, respectively, and the chemical shift value of $^{1}H^{N}_{i}$ in a direct time domain dimension, $t_3(^{1}H^{N})$, and (2) to cosine modulate the $^{13}C^{\alpha}_{i-1}$ chemical shift evolution in $t_1(^{13}C^{\alpha})$ with the chemical shift evolution of $^{1}H^{\alpha}_{i-1}$; and

processing the NMR signals to generate a 3D NMR spectrum with a primary peak pair derived from said cosine modulating, wherein (1) the chemical shift values of $^{15}N_i$ and $^{1}H^{N}_{i}$ are measured in two frequency domain dimensions, $\omega_2(^{15}N)$ and $\omega_3(^{1}H^{N})$, respectively, and (2) the chemical shift values of $^{1}H^{\alpha}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha})$, by the frequency difference between the two peaks forming said primary peak pair and the frequency at the center of the two peaks, respectively.

2. The method according to claim 1, wherein said applying radiofrequency pulses is carried out so that the chemical shift evolution of $^{15}N_i$ does not occur and said processing the NMR signals generates a two dimensional (2D) NMR spectrum with a peak pair wherein (1) the chemical shift value of $^{1}H^{N}_{i}$ is measured in a frequency domain dimension, $\omega_2(^{1}H^{N})$, and (2) the chemical shift values of $^{1}H^{\alpha}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha})$, by the frequency difference between the two peaks forming said primary peak pair and the frequency at the center of the two peaks, respectively.

3. The method according to claim 1, wherein said applying radiofrequency pulses is carried out so that the chemical shift evolution of a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$, occurs under conditions effective to generate NMR signals encoding the chemical shift value of $^{13}C'_{i-1}$ in a phase sensitive manner in an indirect time domain dimension, $t_4(^{13}C')$, and said processing the NMR signals generates a four dimensional (4D) NMR spectrum with a peak pair wherein (1) the chemical shift values of $^{15}N_i$, $^{1}H^{N}_{i}$ and $^{13}C'_{i-1}$ are measured in three frequency domain dimensions, $\omega_2(^{15}N)$, $\omega_3(^{1}H^{N})$, and $\omega_4(^{13}C')$, respectively, and (2) the chemical shift values of $^{1}H^{\alpha}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha})$, by the frequency difference between the two peaks forming said peak pair and the frequency at the center of the two peaks, respectively.

4. The method according to claim 1, wherein said applying radiofrequency pulses is carried out under conditions effective to additionally cosine modulate the $^{13}C^{\alpha}_{i-1}$ chemical shift evolution in $t_1(^{13}C^{\alpha})$ with the chemical shift evolution of a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$, and said processing the NMR signals generates a 3D NMR spectrum with two secondary peak pairs wherein (1) each of the secondary peak pairs is derived from a different one of the peaks of the primary peak pair, and (2) the chemical shift value of $^{13}C'_{i-1}$ is measured along $\omega_1(^{13}C^{\alpha})$ by the frequency difference between the two peaks forming one of the secondary peak pairs.

5. The method according to claim 4, wherein said applying radiofrequency pulses is carried out under conditions effective (1) to generate an additional NMR signal encoding the chemical shift values of $^{13}C^{\alpha}_{i-1}$ and $^{15}N_i$ in a phase sensitive manner in $t_1(^{13}C^{\alpha})$ and $t_2(^{15}N)$ and the chemical shift value of $^{1}H^{N}_{i}$ in $t_3(^{1}H^{N})$, (2) to cosine modulate the $^{13}C^{\alpha}_{i-1}$ chemical shift evolution in $t_1(^{13}C^{\alpha})$ with the chemical shift evolution of $^{13}C'_{i-1}$, and (3) to avoid cosine modulating the $^{13}C^{\alpha}_{i-1}$ chemical shift evolution in $t_1(^{13}C^{\alpha})$ with the chemical shift evolution of $^{1}H^{\alpha}_{i-1}$, and said processing the NMR signals and the additional NMR signal generates a 3D NMR spectrum with an additional secondary peak pair located between said two secondary peak pairs which measures the chemical shift values of $^{13}C'_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ along $\omega_1(^{13}C^{\alpha})$, by the frequency difference between the two peaks forming the additional secondary peak pair and the frequency at the center of said two peaks, respectively.

6. The method according to claim 5, wherein said additional secondary peak pair is derived from $^{13}C^{\alpha}$ nuclear spin polarization.

7. The method according to claim 6, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1B, wherein a radiofrequency pulse is used to create transverse $^{1}H^{\alpha}_{i-1}$ magnetization, and $^{1}H^{\alpha}_{i-1}$ magnetization is transferred to $^{13}C^{\alpha}_{i-1}$, to $^{15}N_i$, and to $^{1}H^{N}_{i}$, where the NMR signal is detected.

8. The method according to claim 7, wherein said applying radiofrequency pulses comprises:

applying a first set of radiofrequency pulses according to the scheme shown in Figure 2B to generate a first NMR signal, and

applying a second set of radiofrequency pulses according to the scheme shown in Figure 2B, wherein phase ϕ_1 of the first ^{1}H pulse is altered by 180° to generate a second NMR signal, said method further comprising:

adding and subtracting the first NMR signal and the second NMR signal prior to said processing, whereby said processing the NMR signals generates a first NMR subspectrum derived from said subtracting which contains said two secondary peak pairs, and a second NMR subspectrum derived from said adding which contains said additional secondary peak pair.

9. The method according to claim 1, wherein said applying radiofrequency pulses is carried out under conditions effective (1) to generate an additional NMR signal encoding the chemical shift values of $^{13}C^{\alpha}_{i-1}$ and $^{15}N_i$ in a phase sensitive manner in $t_1(^{13}C^{\alpha})$ and $t_2(^{15}N)$ and the chemical shift value of $^{1}H^{N}_{i}$ in $t_3(^{1}H^{N})$, and (2) to avoid cosine modulating the $^{13}C^{\alpha}_{i-1}$ chemical shift evolution in $t_1(^{13}C^{\alpha})$ with the chemical shift evolution of $^{1}H^{\alpha}_{i-1}$ for the additional NMR signal, and said processing the NMR signals and the additional NMR signal generates a 3D NMR spectrum with an additional peak located centrally between two peaks forming said primary peak pair which measures the chemical shift value of $^{13}C^{\alpha}_{i-1}$ along $\omega_1(^{13}C^{\alpha})$.

10. The method according to claim 9, wherein said additional peak is derived from $^{13}C^{\alpha}$ nuclear spin polarization.

11. The method according to claim 10, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1B, wherein a radiofrequency pulse is used to create transverse $^{1}H^{\alpha}_{i-1}$ magnetization, which is transferred to $^{13}C^{\alpha}_{i-1}$, to $^{15}N_i$, and to $^{1}H^{N}_{i}$, to generate the NMR signal.

12. The method according to claim 11, wherein said applying radiofrequency pulses comprises:

applying a first set of radiofrequency pulses according to the scheme shown in Figure 2B to generate a first NMR signal, and

applying a second set of radiofrequency pulses according to the scheme shown in Figure 2B, wherein phase ϕ_1 of the first ^{1}H pulse is altered by 180° to generate a second NMR signal, said method further comprising:

adding and subtracting the first NMR signal and the second NMR signal prior to said processing, whereby said processing the NMR signals generates a first NMR subspectrum derived from said subtracting which contains said primary peak pair and a second NMR subspectrum derived from said adding which contains said additional peak located centrally between the two peaks forming said primary peak pair.

13. A method of conducting a reduced dimensionality three-dimensional (3D) H,C,-(C-TOCSY-CO),N,HN nuclear magnetic resonance (NMR) experiment by measuring the chemical shift values for the following nuclei of a protein molecule having two consecutive amino acid residues, *i*-1 and *i*: (1) aliphatic protons of amino acid residue *i*-1, $^{1}H^{ali}_{i-1}$; (2) aliphatic carbons of amino acid residue *i*-1, $^{13}C^{ali}_{i-1}$; (3) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$; and (4) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, said method comprising:

providing a protein sample;

applying radiofrequency pulses to the protein sample which effect a nuclear spin polarization transfer wherein the chemical shift evolutions of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ of amino acid residue *i*-1 are connected to the chemical shift evolutions of $^{15}N_i$ and $^{1}H^{N}_{i}$ of amino acid residue *i*, under conditions effective (1) to generate a NMR signal encoding the chemical

shifts of $^{13}C^{ali}_{i-1}$ and $^{15}N_i$ in a phase sensitive manner in two indirect time domain dimensions, $t_1(^{13}C^{ali})$ and $t_2(^{15}N)$, respectively, and the chemical shift of $^{1}H^{N}_{i}$ in a direct time domain dimension, $t_3(^{1}H^{N})$, and (2) to cosine modulate the chemical shift evolutions of $^{13}C^{ali}_{i-1}$ in $t_1(^{13}C^{ali})$ with the chemical shift evolutions of $^{1}H^{ali}_{i-1}$; and

processing the NMR signals to generate a 3D NMR spectrum with peak pairs derived from said cosine modulating wherein (1) the chemical shift values of $^{15}N_i$ and $^{1}H^{N}_{i}$ are measured in two frequency domain dimensions, $\omega_2(^{15}N)$ and $\omega_3(^{1}H^{N})$, respectively, and (2) the chemical shift values of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{ali})$, by the frequency differences between the two peaks forming said peak pairs and the frequencies at the center of the two peaks, respectively.

14. The method according to claim 13, wherein said applying radiofrequency pulses is carried out so that the chemical shift evolution of $^{15}N_i$ does not occur and said processing the NMR signals generates a two dimensional (2D) NMR spectrum with peak pairs wherein (1) the chemical shift value of $^{1}H^{N}_{i}$ is measured in a frequency domain dimension, $\omega_2(^{1}H^{N})$, and (2) the chemical shift values of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{ali})$, by the frequency differences between the two peaks forming said peak pairs and the frequencies at the center of the two peaks, respectively.

15. The method according to claim 13, wherein said applying radiofrequency pulses is carried out so that the chemical shift evolution of a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$, occurs under conditions effective to generate NMR signals encoding the chemical shift value of $^{13}C'_{i-1}$ in a phase sensitive manner in an indirect time domain dimension, $t_4(^{13}C')$, and said processing the NMR signals generates a four dimensional (4D) NMR spectrum with variant peak pairs wherein (1) the chemical shift values of $^{15}N_i$, $^{1}H^{N}_{i}$ and $^{13}C'_{i-1}$ are measured in three frequency domain dimensions, $\omega_2(^{15}N)$, $\omega_3(^{1}H^{N})$, and $\omega_4(^{13}C')$, respectively, and (2) the chemical shift values of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{ali})$, by the frequency differences between the two peaks forming said variant peak pairs and the frequencies at the center of the two peaks, respectively.

16. The method according to claim 13, wherein said applying radiofrequency pulses is carried out under conditions effective (1) to generate an additional NMR signal

encoding the chemical shift values of $^{13}C^{ali}_{i-1}$ and $^{15}N_i$ in a phase sensitive manner in $t_1(^{13}C^{ali})$ and $t_2(^{15}N)$ and the chemical shift value of $^{1}H^{N}_{i}$ in $t_3(^{1}H^{N})$, and (2) to avoid cosine modulating the chemical shift evolutions of $^{13}C^{ali}_{i-1}$ in $t_1(^{13}C^{ali})$ with the chemical shift evolution of $^{1}H^{\alpha}_{i-1}$ for the additional NMR signal, and said processing the NMR signals and the additional NMR signal generates a 3D NMR spectrum with additional peaks located centrally between said peak pairs which measure the chemical shift values of $^{13}C^{ali}_{i-1}$ along $\omega_1(^{13}C^{ali})$.

17. The method according to claim 16, wherein said additional peaks are derived from $^{13}C^{ali}$ nuclear spin polarization.

18. The method according to claim 17, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1C, wherein a radiofrequency pulse is used to create transverse $^{1}H^{ali}_{i-1}$ magnetization, and $^{1}H^{ali}_{i-1}$ magnetization is transferred to $^{13}C^{ali}_{i-1}$, to $^{13}C^{\alpha}_{i-1}$, to $^{13}C'_{i-1}$, to $^{15}N_i$, and to $^{1}H^{N}_{i}$, where the NMR signal is detected.

19. The method according to claim 18, wherein said applying radiofrequency pulses comprises:

applying a first set of radiofrequency pulses according to the scheme shown in Figure 2C to generate a first NMR signal, and

applying a second set of radiofrequency pulses according to the scheme shown in Figure 2C, wherein phase ϕ_1 of the first ^{1}H pulse is altered by 180° to generate a second NMR signal, said method further comprising:

adding and subtracting the first NMR signal and the second NMR signal prior to said processing, whereby said processing the NMR signals generates a first NMR subspectrum derived from said subtracting which contains said peak pairs, and a second NMR subspectrum derived from said adding which contains said additional peaks located centrally between said peak pairs.

20. A method of conducting a reduced dimensionality three-dimensional (3D) $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,CO,HA nuclear magnetic resonance (NMR) experiment by measuring the chemical shift values for the following nuclei of a protein molecule having an amino acid residue, *i*: (1) a β-proton of amino acid residue *i*, $^{1}H^{\beta}_{i}$; (2) a β-carbon of amino acid residue *i*, $^{13}C^{\beta}_{i}$; (3) an

α-proton of amino acid residue *i*, $^{1}H^{\alpha}_{i}$; (4) an α-carbon of amino acid residue *i*, $^{13}C^{\alpha}_{i}$; and (5) a polypeptide backbone carbonyl carbon of amino acid residue *i*, $^{13}C'_{i}$, said method comprising:

providing a protein sample;

applying radiofrequency pulses to the protein sample which effect a nuclear spin polarization transfer wherein the chemical shift evolutions of $^{1}H^{\alpha}_{i}$, $^{1}H^{\beta}_{i}$, $^{13}C^{\alpha}_{i}$, and $^{13}C^{\beta}_{i}$ are connected to the chemical shift evolution of $^{13}C'_{i}$, under conditions effective (1) to generate NMR signals encoding the chemical shift values of $^{13}C^{\alpha}_{i}$, $^{13}C^{\beta}_{i}$ and $^{13}C'_{i}$ in a phase sensitive manner in two indirect time domain dimensions, $t_1(^{13}C^{\alpha/\beta})$ and $t_2(^{13}C')$, respectively, and the chemical shift value of $^{1}H^{\alpha}_{i}$ in a direct time domain dimension, $t_3(^{1}H^{\alpha})$, and (2) to cosine modulate the chemical shift evolutions of $^{13}C^{\alpha}_{i}$ and $^{13}C^{\beta}_{i}$ in $t_1(^{13}C^{\alpha/\beta})$ with the chemical shift evolutions of $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$, respectively; and

processing the NMR signals to generate a 3D NMR spectrum with peak pairs derived from said cosine modulating wherein (1) the chemical shift values of $^{13}C'_{i}$ and $^{1}H^{\alpha}_{i}$ are measured in two frequency domain dimensions, $\omega_2(^{13}C')$ and $\omega_3(^{1}H^{\alpha})$, respectively, and (2) (i) the chemical shift values of $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha/\beta})$, by the frequency differences between the two peaks forming said peak pairs, and (ii) the chemical shift values of $^{13}C^{\alpha}_{i}$, and $^{13}C^{\beta}_{i}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha/\beta})$, by the frequencies at the center of the two peaks forming said peak pairs.

21. The method according to claim 20, wherein said applying radiofrequency pulses is carried out so that the chemical shift evolution of $^{13}C'_{i}$ does not occur and said processing the NMR signals generates a two dimensional (2D) NMR spectrum with peak pairs wherein (1) the chemical shift value of $^{1}H^{\alpha}_{i}$ is measured in a frequency domain dimension, $\omega_2(^{1}H^{\alpha})$, and (2) (i) the chemical shift values of $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha/\beta})$, by the frequency differences between two peaks forming said peak pairs, respectively, and (ii) the chemical shift values of $^{13}C^{\alpha}_{i}$, and $^{13}C^{\beta}_{i}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha/\beta})$, by the frequencies at the center of the two peaks forming said peak pairs.

22. The method according to claim 20 wherein said applying radiofrequency pulses is carried out under conditions effective (1) to generate an additional NMR signal encoding the chemical shift values of $^{13}C^{\alpha}_{i}$, $^{13}C^{\beta}_{i}$ and $^{15}N_{i}$ in a phase sensitive manner in $t_1(^{13}C^{\alpha/\beta})$ and $t_2(^{15}N)$ and the chemical shift value of $^{1}H^{\alpha}_{i}$ in $t_3(^{1}H^{\alpha})$, and (2) to avoid cosine modulating the chemical shift evolutions of $^{13}C^{\alpha}_{i}$ and $^{13}C^{\beta}_{i}$ in $t_1(^{13}C^{\alpha/\beta})$ with the chemical shift evolutions of $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$ for the additional NMR signal, and said processing the NMR signals and the additional NMR signal generates a 3D NMR spectrum with additional peaks located centrally between the two peaks forming said peak pairs which measure the chemical shift values of $^{13}C^{\alpha}_{i}$ and $^{13}C^{\beta}_{i}$ along $\omega_1(^{13}C^{\alpha/\beta})$.

23. The method according to claim 22, wherein said additional peaks are derived from $^{13}C^{\alpha}$ and $^{13}C^{\beta}$ nuclear spin polarization.

24. The method according to claim 23, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1E, wherein a radiofrequency pulse is used to create transverse $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$ magnetization, and $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$ polarization is transferred to $^{13}C^{\alpha}_{i}$ and $^{13}C^{\beta}_{i}$, to $^{13}C'_{i}$, and back to $^{1}H^{\alpha}_{i}$, where the NMR signal is detected.

25. The method according to claim 24, wherein said applying radiofrequency pulses comprises:

applying a first set of radiofrequency pulses according to the scheme shown in Figure 2E to generate a first NMR signal, and

applying a second set of radiofrequency pulses according to the scheme shown in Figure 2E, wherein phase ϕ_1 of the first ^{1}H pulse is altered by 180° to generate a second NMR signal, said method further comprising:

adding and subtracting the first NMR signal and the second NMR signal prior to said processing, whereby said processing the NMR signals generates a first NMR subspectrum derived from said subtracting which contains said peak pairs, and a second NMR subspectrum derived from said adding which contains said additional peaks located centrally between the two peaks forming said peak pairs.

26. A method of conducting a reduced dimensionality three-dimensional (3D) $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,N,HN nuclear magnetic resonance (NMR) experiment by measuring the chemical shift values for the following nuclei of a protein molecule having an amino acid residue, *i*: (1) a β-proton of amino acid residue *i*, $^{1}H^{\beta}_{i}$; (2) a β-carbon of amino acid residue *i*, $^{13}C^{\beta}_{i}$; (3) an α-proton of amino acid residue *i*, $^{1}H^{\alpha}_{i}$; (4) an α-carbon of amino acid residue *i*, $^{13}C^{\alpha}_{i}$; (5) a polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_{i}$; and (6) a polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$, said method comprising:

providing a protein sample;

applying radiofrequency pulses to the protein sample which effect a nuclear spin polarization transfer wherein the chemical shift evolutions of $^{1}H^{\alpha}_{i}$, $^{1}H^{\beta}_{i}$, $^{13}C^{\alpha}_{i}$, and $^{13}C^{\beta}_{i}$ are connected to the chemical shift evolutions of $^{15}N_{i}$ and $^{1}H^{N}_{i}$, under conditions effective (1) to generate NMR signals encoding the chemical shift values of $^{13}C^{\alpha}_{i}$, $^{13}C^{\beta}_{i}$ and $^{15}N_{i}$ in a phase sensitive manner in two indirect time domain dimensions, $t_1(^{13}C^{\alpha/\beta})$ and $t_2(^{15}N)$, respectively, and the chemical shift value of $^{1}H^{N}_{i}$ in a direct time domain dimension, $t_3(^{1}H^{N})$, and (2) to cosine modulate the chemical shift evolutions of $^{13}C^{\alpha}_{i}$ and $^{13}C^{\beta}_{i}$ in $t_1(^{13}C^{\alpha/\beta})$ with the chemical shift evolutions of $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$, respectively; and

processing the NMR signals to generate a 3D NMR spectrum with peak pairs derived from said cosine modulating wherein (1) the chemical shift values of $^{15}N_{i}$ and $^{1}H^{N}_{i}$ are measured in two frequency domain dimensions, $\omega_2(^{15}N)$ and $\omega_3(^{1}H^{N})$, respectively, and (2) (i) the chemical shift values of $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha/\beta})$, by the frequency differences between the two peaks forming said peak pairs, and (ii) the chemical shift values of $^{13}C^{\alpha}_{i}$, and $^{13}C^{\beta}_{i}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha/\beta})$, by the frequencies at the center of said two peaks forming said peak pairs.

27. The method according to claim 26, wherein said applying radiofrequency pulses is carried out so that the chemical shift evolution of $^{15}N_{i}$ does not occur and said processing the NMR signals generates a two dimensional (2D) NMR spectrum with peak pairs wherein (1) the chemical shift value of $^{1}H^{N}_{i}$ is measured in a frequency domain dimension, $\omega_2(^{1}H^{N})$, and (2) (i) the chemical shift values of $^{1}H^{\alpha}_{i}$ and $^{1}H^{\beta}_{i}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\alpha/\beta})$, by the frequency differences between the two peaks forming said peak pairs, and (ii) the chemical shift values of $^{13}C^{\alpha}_{i}$, and $^{13}C^{\beta}_{i}$ are measured in a

frequency domain dimension, $\omega_1(^{13}C^{\alpha/\beta})$, by the frequencies at the center of the two peaks forming said peak pairs.

28. The method according to claim 26, wherein said applying radiofrequency pulses is carried out under conditions effective (1) to generate an additional NMR signal encoding the chemical shift values of $^{13}C^{\alpha}_i$, $^{13}C^{\beta}_i$ and $^{15}N_i$ in a phase sensitive manner in $t_1(^{13}C^{\alpha/\beta})$ and $t_2(^{15}N)$ and the chemical shift value of $^{1}H^{N}_i$ in $t_3(^{1}H^{N})$, and (2) to avoid cosine modulating the chemical shift evolutions of $^{13}C^{\alpha}_i$ and $^{13}C^{\beta}_i$ in $t_1(^{13}C^{\alpha/\beta})$ with the chemical shift evolutions of $^{1}H^{\alpha}_i$ and $^{1}H^{\beta}_i$ for the additional NMR signal, and said processing the NMR signals and the additional NMR signal generates a 3D NMR spectrum with additional peaks located centrally between the two peaks forming said peak pairs which measure the chemical shift values of $^{13}C^{\alpha}_i$ and $^{13}C^{\beta}_i$ along $\omega_1(^{13}C^{\alpha/\beta})$.

29. The method according to claim 28, wherein said additional peaks are derived from $^{13}C^{\alpha}$ and $^{13}C^{\beta}$ nuclear spin polarization.

30. The method according to claim 29, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1F, wherein a radiofrequency pulse is used to create transverse $^{1}H^{\alpha}_i$ and $^{1}H^{\beta}_i$ magnetization, and $^{1}H^{\alpha}_i$ and $^{1}H^{\beta}_i$ magnetization is transferred to $^{13}C^{\alpha}_i$ and $^{13}C^{\beta}_i$, to $^{15}N_i$, and to $^{1}H^{N}_i$, where the NMR signal is detected.

31. The method according to claim 30, wherein said applying radiofrequency pulses comprises:

applying a first set of radiofrequency pulses according to the scheme shown in Figure 2F to generate a first NMR signal, and

applying a second set of radiofrequency pulses according to the scheme shown in Figure 2F, wherein phase ϕ_1 of the first ^{1}H pulse is altered by 180° to generate a second NMR signal, said method further comprising:

adding and subtracting the first NMR signal and the second NMR signal prior to said processing, whereby said processing the NMR signals generates a first NMR subspectrum derived from said subtracting which contains said peak pairs, and a second

NMR subspectrum derived from said adding which contains said additional peaks located centrally between the two peaks forming said peak pairs.

32. A method of conducting a reduced dimensionality three-dimensional (3D) H,C,C,H-COSY nuclear magnetic resonance (NMR) experiment by measuring the chemical shift values for $^{1}H^{m}$, $^{13}C^{m}$, $^{1}H^{n}$, and $^{13}C^{n}$ of a protein molecule wherein m and n indicate atom numbers of two CH, CH_2 or CH_3 groups that are linked by a single covalent carbon-carbon bond in an amino acid residue, said method comprising:

providing a protein sample;

applying radiofrequency pulses to the protein sample which effect a nuclear spin polarization transfer wherein the chemical shift evolutions of $^{1}H^{m}$ and $^{13}C^{m}$ are connected to the chemical shift evolutions of $^{1}H^{n}$ and $^{13}C^{n}$, under conditions effective (1) to generate NMR signals encoding the chemical shift values of $^{13}C^{m}$ and $^{13}C^{n}$ in a phase sensitive manner in two indirect time domain dimensions, $t_1(^{13}C^{m})$ and $t_2(^{13}C^{n})$, respectively, and the chemical shift value of $^{1}H^{n}$ in a direct time domain dimension, $t_3(^{1}H^{n})$, and (2) to cosine modulate the chemical shift evolution of $^{13}C^{m}$ in $t_1(^{13}C^{m})$ with the chemical shift evolution of $^{1}H_{m}$; and

processing the NMR signals to generate a 3D NMR spectrum with peak pairs derived from said cosine modulating wherein (1) the chemical shift values of $^{13}C^{n}$ and $^{1}H^{n}$ are measured in two frequency domain dimensions, $\omega_2(^{13}C^{n})$ and $\omega_3(^{1}H^{n})$, respectively, and (2) the chemical shift values of $^{1}H^{m}$ and $^{13}C^{m}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{m})$, by the frequency differences between the two peaks forming said peak pairs and the frequencies at the center of the two peaks, respectively.

33. The method according to claim 32, wherein said applying radiofrequency pulses is carried out so that the chemical shift evolution of $^{13}C^{n}$ does not occur and said processing the NMR signals generates a two dimensional (2D) NMR spectrum with peak pairs wherein (1) the chemical shift value of $^{1}H^{n}$ is measured in a frequency domain dimension, $\omega_2(^{1}H^{n})$, and (2) the chemical shift values of $^{1}H^{m}$ and $^{13}C^{m}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{m})$, by the frequency differences between the two peaks forming said peak pairs and the frequencies at the center of the two peaks, respectively.

34. The method according to claim 32, wherein said applying radiofrequency pulses is carried out under conditions effective (1) to generate an additional NMR signal encoding the chemical shift values of $^{13}C^m$ and $^{13}C^n$ in a phase sensitive manner in $t_1(^{13}C^m)$ and $t_2(^{13}C^n)$ and the chemical shift value of $^1H^n$ in $t_3(^1H)$, and (2) to avoid cosine modulating the chemical shift evolution of $^{13}C^m$ in $t_1(^{13}C^m)$ with the chemical shift evolution of $^1H^m$ for the additional NMR signal, and said processing the NMR signals and the additional NMR signal generates a 3D NMR spectrum with additional peaks located centrally between the two peaks forming said peak pairs which measure the chemical shift value of $^{13}C^m$ along $\omega_1(^{13}C^m)$.

35. The method according to claim 34, wherein said additional peaks are derived from $^{13}C^m$ nuclear spin polarization.

36. The method according to claim 35, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1H, wherein a radiofrequency pulse is used to create transverse $^1H^m$ magnetization, and $^1H^m$ magnetization is transferred to $^{13}C^m$, to $^{13}C^n$, and to $^1H^n$, where the NMR signal is detected.

37. The method according to claim 36, wherein said applying radiofrequency pulses comprises:

applying a first set of radiofrequency pulses according to the scheme shown in Figure 2H to generate a first NMR signal, and

applying a second set of radiofrequency pulses according to the scheme shown in Figure 2H, wherein phase ϕ_1 of the first ^1H pulse is altered by 180° to generate a second NMR signal, said method further comprising:

adding and subtracting the first NMR signal and the second NMR signal prior to said processing, whereby said processing the NMR signals generates a first NMR subspectrum derived from said subtracting which contains said peak pairs, and a second NMR subspectrum derived from said adding which contains said additional peaks located centrally between the two peaks forming said peak pairs.

38. A method of conducting a reduced dimensionality three-dimensional (3D) H,C,C,H-TOCSY nuclear magnetic resonance (NMR) experiment by measuring the chemical shift values for $^1H^m$, $^{13}C^m$, $^1H^n$, and $^{13}C^n$ of a protein molecule wherein *m* and *n* indicate atom

numbers of two CH, CH_2 or CH_3 groups that may or may not be directly linked by a single covalent carbon-carbon bond in an amino acid residue, said method comprising:

providing a protein sample;

applying radiofrequency pulses to the protein sample which effect a nuclear spin polarization transfer wherein the chemical shift evolutions of $^1H^m$ and $^{13}C^m$ are connected to the chemical shift evolutions of $^1H^n$ and $^{13}C^n$, under conditions effective (1) to generate NMR signals encoding the chemical shift values of $^{13}C^m$ and $^{13}C^n$ in a phase sensitive manner in two indirect time domain dimensions, $t_1(^{13}C^m)$ and $t_2(^{13}C^n)$, and the chemical shift value of $^1H^n$ in a direct time domain dimension, $t_3(^1H^n)$, and (2) to cosine modulate the chemical shift evolution of $^{13}C^m$ in $t_1(^{13}C^m)$ with the chemical shift evolution of $^1H^m$; and

processing the NMR signals to generate a 3D NMR spectrum with peak pairs derived from said cosine modulating wherein (1) the chemical shift values of $^{13}C^n$ and $^1H^n$ are measured in two frequency domain dimensions, $\omega_2(^{13}C^n)$ and $\omega_3(^1H^n)$, respectively, and (2) the chemical shift values of $^1H^m$ and $^{13}C^m$ are measured in a frequency domain dimension, $\omega_1(^{13}C^m)$, by the frequency differences between the two peaks forming said peak pairs and the frequencies at the center of the two peaks, respectively.

39. The method according to claim 38, wherein said applying radiofrequency pulses is carried out so that the chemical shift evolution of $^{13}C^n$ does not occur and said processing the NMR signals generates a two dimensional (2D) NMR spectrum with peak pairs wherein (1) the chemical shift value of $^1H^n$ is measured in a frequency domain dimension, $\omega_2(^1H^n)$, and (2) the chemical shift values of $^1H^m$ and $^{13}C^m$ are measured in a frequency domain dimension, $\omega_1(^{13}C^m)$, by the frequency differences between the two peaks forming said peak pairs and the frequencies at the center of the two peaks, respectively.

40. The method according to claim 38, wherein said applying radiofrequency pulses is carried out under conditions effective (1) to generate an additional NMR signal encoding the chemical shift values of $^{13}C^m$ and $^{13}C^n$ in a phase sensitive manner in $t_1(^{13}C^m)$ and $t_2(^{13}C^n)$ and the chemical shift value of $^1H^n$ in $t_3(^1H^n)$, and (2) to avoid cosine modulating the chemical shift evolution of $^{13}C^m$ in $t_1(^{13}C^m)$ with the chemical shift evolution of $^1H^m$ for the additional NMR signal, and said processing the NMR signals and the additional NMR

signal generates a 3D NMR spectrum with additional peaks located centrally between the two peaks forming said peak pairs which measure the chemical shift value of $^{13}C^{m}$ along $\omega_1(^{13}C^{m})$.

41. The method according to claim 40, wherein said additional peaks are derived from $^{13}C^{m}$ nuclear spin polarization.

42. The method according to claim 41, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1I, wherein a radiofrequency pulse is used to create transverse $^{1}H^{m}$ magnetization, and $^{1}H^{m}$ magnetization is transferred to $^{13}C^{m}$, to $^{13}C^{n}$, and to $^{1}H^{n}$, where the NMR signal is detected.

43. The method according to claim 42, wherein said applying radiofrequency pulses comprises:

applying a first set of radiofrequency pulses according to the scheme shown in Figure 2I to generate a first NMR signal, and

applying a second set of radiofrequency pulses according to the scheme shown in Figure 2I, wherein phase ϕ_1 of the first ^{1}H pulse is altered by 180° to generate a second NMR signal, said method further comprising:

adding and subtracting the first NMR signal and the second NMR signal prior to said processing, whereby said processing the NMR signals generates a first NMR subspectrum derived from said subtracting which contains said peak pairs, and a second NMR subspectrum derived from said adding which contains said additional peaks located centrally between the two peaks forming said peak pairs.

44. A method of conducting a reduced dimensionality two-dimensional (2D) HB,CB,(CG,CD),HD nuclear magnetic resonance (NMR) experiment by measuring the chemical shift values for the following nuclei of a protein molecule : (1) a β-proton of an amino acid residue with an aromatic side chain, $^{1}H^{\beta}$; (2) a β-carbon of an amino acid residue with an aromatic side chain, $^{13}C^{\beta}$; and (3) a δ-proton of an amino acid residue with an aromatic side chain, $^{1}H^{\delta}$, said method comprising:

providing a protein sample;

applying radiofrequency pulses to the protein sample which effect a nuclear spin polarization transfer wherein the chemical shift evolutions of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ are connected

to the chemical shift evolution of $^{1}H^{\delta}$, under conditions effective (1) to generate NMR signals encoding the chemical shift value of $^{13}C^{\beta}$ in a phase sensitive manner in an indirect time domain dimension, $t_1(^{13}C^{\beta})$, and the chemical shift value of $^{1}H^{\delta}$ in a direct time domain dimension, $t_2(^{1}H^{\delta})$, and (2) to cosine modulate the chemical shift evolution of $^{13}C^{\beta}$ in $t_1(^{13}C^{\beta})$ with the chemical shift evolution of $^{1}H^{\beta}$; and

processing the NMR signals to generate a 2D NMR spectrum with a peak pair derived from said cosine modulating wherein (1) the chemical shift value of $^{1}H^{\delta}$ is measured in a frequency domain dimension, $\omega_2(^{1}H^{\delta})$, and (2) the chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\beta})$, by the frequency difference between the two peaks forming said peak pair and the frequency at the center of the two peaks, respectively.

45. The method according to claim 44, wherein said applying radiofrequency pulses is carried out so that:

(i) the chemical shift evolution of a δ-carbon of an amino acid residue with an aromatic side chain, $^{13}C^{\delta}$, occurs under conditions effective to generate NMR signals encoding the chemical shift value of $^{13}C^{\delta}$ in a phase sensitive manner in an indirect time domain dimension, $t_3(^{13}C^{\delta})$, and said processing the NMR signals generates a three dimensional (3D) NMR spectrum with a peak pair wherein (1) the chemical shift values of $^{1}H^{\delta}$ and $^{13}C^{\delta}$ are measured in two frequency domain dimensions, $\omega_2(^{1}H^{\delta})$ and $\omega_3(^{13}C^{\delta})$, respectively, and (2) the chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\beta})$, by the frequency difference between the two peaks forming said peak pair and the frequency at the center of the two peaks, respectively; or

(ii) the chemical shift evolution of a γ-carbon of an amino acid residue with an aromatic side chain, $^{13}C^{\gamma}$ occurs under conditions effective to generate NMR signals encoding the chemical shift value of $^{13}C^{\gamma}$, in a phase sensitive manner in an indirect time domain dimension, $t_3(^{13}C^{\gamma})$, and said processing the NMR signals generates a three dimensional (3D) NMR spectrum with a peak pair wherein (1) the chemical shift values of $^{1}H^{\delta}$ and $^{13}C^{\gamma}$ are measured in two frequency domain dimensions, $\omega_2(^{1}H^{\delta})$ and $\omega_3(^{13}C^{\gamma})$, respectively, and (2) the chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{\beta})$, by the frequency difference between the two peaks forming said peak pair and the frequency at the center of the two peaks, respectively.

46. The method according to claim 44, wherein said applying radiofrequency pulses is carried out under conditions effective (1) to generate an additional NMR signal encoding the chemical shift value of $^{13}C^{\beta}$ in a phase sensitive manner in $t_1(^{13}C^{\beta})$ and the chemical shift value of $^{1}H^{\delta}$ in $t_2(^{1}H^{\delta})$, and (2) to avoid cosine modulating the chemical shift evolution of $^{13}C^{\beta}$ in $t_1(^{13}C^{\beta})$ with the chemical shift evolution of $^{1}H^{\beta}$ for the additional NMR signal, and said processing the NMR signals and the additional NMR signal generates a 2D NMR spectrum with an additional peak located centrally between said peak pair which measure the chemical shift value of $^{13}C^{\beta}$ along $\omega_1(^{13}C^{\beta})$.

47. The method according to claim 46, wherein said additional peak is derived from $^{13}C^{\beta}$ nuclear spin polarization.

48. The method according to claim 47, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1J, wherein a radiofrequency pulse is used to create transverse $^{1}H^{\beta}$ magnetization, and $^{1}H^{\beta}$ magnetization is transferred to $^{13}C^{\beta}$, to $^{13}C^{\delta}$, and to $^{1}H^{\delta}$, where the NMR signal is detected.

49. The method according to claim 48, wherein said applying radiofrequency pulses comprises:

applying a first set of radiofrequency pulses according to the scheme shown in Figure 2J to generate a first NMR signal, and

applying a second set of radiofrequency pulses according to the scheme shown in Figure 2J, wherein phase ϕ_1 of the first ^{1}H pulse is altered by 180° to generate a second NMR signal, said method further comprising:

adding and subtracting the first NMR signal and the second NMR signal prior to said processing, whereby said processing the NMR signals generates a first NMR subspectrum derived from said subtracting which contains said peak pair, and a second NMR subspectrum derived from said adding which contains said additional peak located centrally between the two peaks forming said peak pair.

50. A method of conducting a reduced dimensionality two-dimensional (2D) H,C,H-COSY nuclear magnetic resonance (NMR) experiment by measuring the chemical

shift values for $^{1}H^{m}$, $^{13}C^{m}$, and $^{1}H^{n}$ of a protein molecule wherein *m* and *n* indicate atom numbers of two CH, CH_2 or CH_3 groups in an amino acid residue, said method comprising:

providing a protein sample;

applying radiofrequency pulses to the protein sample which effect a nuclear spin polarization transfer wherein the chemical shift evolutions of $^{1}H^{m}$ and $^{13}C^{m}$ are connected to the chemical shift evolution of $^{1}H^{n}$, under conditions effective (1) to generate NMR signals encoding the chemical shift value of $^{13}C^{m}$ in a phase sensitive manner in an indirect time domain dimension, $t_1(^{13}C^{m})$, and the chemical shift value of $^{1}H^{n}$ in a direct time domain dimension, $t_2(^{1}H^{n})$, and (2) to cosine modulate the chemical shift evolution of $^{13}C^{m}$ in $t_1(^{13}C^{m})$ with the chemical shift evolution of $^{1}H^{m}$; and

processing the NMR signals to generate a 2D NMR spectrum with peak pairs derived from said cosine modulating wherein (1) the chemical shift value of $^{1}H^{n}$ is measured in a frequency domain dimension, $\omega_2(^{1}H^{n})$, and (2) the chemical shift values of $^{1}H^{m}$ and $^{13}C^{m}$ are measured in a frequency domain dimension, $\omega_1(^{13}C^{m})$, by the frequency differences between the two peaks forming said peak pairs and the frequencies at the center of the two peaks, respectively.

51. The method according to claim 50, wherein said applying radiofrequency pulses effects a nuclear spin polarization transfer according to Figure 1K, wherein a radiofrequency pulse is used to create transverse $^{1}H^{m}$ magnetization, and $^{1}H^{m}$ polarization is transferred to $^{13}C^{m}$, to $^{1}H^{m}$, and to $^{1}H^{n}$, where the NMR signal is detected.

52. The method according to claim 51, wherein said applying radiofrequency pulses is carried out according to the scheme shown in Figure 2K.

53. A method for sequentially assigning chemical shift values of an α-proton, $^{1}H^{\alpha}$, an α-carbon, $^{13}C^{\alpha}$, a polypeptide backbone amide nitrogen, ^{15}N, and a polypeptide backbone amide proton, $^{1}H^{N}$, of a protein molecule comprising:

providing a protein sample;

conducting a set of reduced dimensionality (RD) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a RD three dimensional (3D) HA,CA,(CO),N,HN NMR experiment to measure and connect chemical shift values of the α-proton of amino acid residue *i*-1, $^{1}H^{\alpha}_{i-1}$, the α-carbon of amino acid residue *i*-1, $^{13}C^{\alpha}_{i-1}$, the

polypeptide backbone amide nitrogen of amino acid residue *i*, $^{15}N_i$, and the polypeptide backbone amide proton of amino acid residue *i*, $^{1}H^{N}_{i}$ and (2) a RD 3D HNN<u>CAHA</u> NMR experiment to measure and connect the chemical shift values of the α-proton of amino acid residue *i*, $^{1}H^{\alpha}_{i}$, the α-carbon of amino acid residue *i*, $^{13}C^{\alpha}_{i}$, $^{15}N_i$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{\alpha}$, $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ by (i) matching the chemical shift values of $^{1}H^{\alpha}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ with the chemical shift values of $^{1}H^{\alpha}_{i}$ and $^{13}C^{\alpha}_{i}$, (ii) using the chemical shift values of $^{1}H^{\alpha}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ to identify the type of amino acid residue *i*-1, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and using said chemical shift values to locate secondary structure elements within the polypeptide chain.

54. The method according to claim 53 further comprising:

subjecting the protein sample to a RD 3D $\underline{H}^{\alpha/\beta}\underline{C}^{\alpha/\beta}$(CO)NHN NMR experiment to measure and connect the chemical shift values of the β-proton of amino acid residue *i*-1, $^{1}H^{\beta}_{i-1}$, the β-carbon of amino acid residue *i*-1, $^{13}C^{\beta}_{i-1}$, $^{1}H^{\alpha}_{i-1}$, $^{13}C^{\alpha}_{i-1}$, $^{15}N_i$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ by using the chemical shift values of $^{1}H^{\beta}_{i-1}$ and $^{13}C^{\beta}_{i-1}$ to identify the type of amino acid residue *i*-1.

55. The method according to claim 54 further comprising:

subjecting the protein sample to a RD 3D $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,CO,HA NMR experiment to measure and connect the chemical shift values of the β-proton of amino acid residue *i*, $^{1}H^{\beta}_{i}$, the β-carbon of amino acid residue *i*, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, $^{13}C^{\alpha}_{i}$, and a polypeptide backbone carbonyl carbon of amino acid residue *i*, $^{13}C'_{i}$; and

obtaining sequential assignments of the chemical shift value of $^{13}C'_{i}$ by matching the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ measured by said RD 3D $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,CO,HA NMR experiment with the sequentially assigned chemical shift values of $^{1}H^{\beta}$, $^{13}C^{\beta}$, $^{1}H^{\alpha}$, $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ measured by said RD 3D <u>HA,CA</u>,(CO),N,HN NMR experiment, RD 3D HNN<u>CAHA</u> NMR experiment, and RD 3D $\underline{H}^{\alpha/\beta}\underline{C}^{\alpha/\beta}$(CO)NHN NMR experiment.

56. The method according to claim 54 further comprising:

subjecting the protein sample to a RD 3D $\underline{H}^{\alpha/\beta},\underline{C}^{\alpha/\beta}$,N,HN NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments by matching the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ with the chemical shift values of $^{1}H^{\beta}_{i-1}$, $^{13}C^{\beta}_{i-1}$, $^{1}H^{\alpha}_{i-1}$, and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D $\underline{H}^{\alpha/\beta}\underline{C}^{\alpha/\beta}$(CO)NHN NMR experiment.

57. The method according to claim 54 further comprising:

subjecting the protein sample to a 3D HNNCACB NMR experiment to measure and connect the chemical shift value of $^{13}C^{\beta}_{i}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments by matching the chemical shift values of $^{13}C^{\beta}_{i}$ and $^{13}C^{\alpha}_{i}$ measure by said 3D HNNCACB NMR experiment with the chemical shift values of $^{13}C^{\beta}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D $\underline{H}^{\alpha/\beta}\underline{C}^{\alpha/\beta}$(CO)NHN NMR experiment.

58. The method according to claim 54 further comprising:

subjecting the protein sample to a RD two-dimensional (2D) HB,CB,(CG,CD),HD NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i-1}$, $^{13}C^{\beta}_{i-1}$, and a δ-proton of amino acid residue i-1 with an aromatic side chain, $^{1}H^{\delta}_{i-1}$; and

obtaining sequential assignments by (i) matching the chemical shift values of $^{1}H^{\beta}_{i-1}$ and $^{13}C^{\beta}_{i-1}$ measured by said RD 2D HB, CB, (CG,CD), HD NMR experiment with the chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ measured by said RD 3D $\underline{H}^{\alpha/\beta}\underline{C}^{\alpha/\beta}$(CO)NHN NMR experiment, (ii) using said chemical shift values to identify amino acid residue i as having an aromatic side chain, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and locating amino acid residues with aromatic side chains along said polypeptide chain.

59. The method according to claim 54 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-COSY NMR experiment or a RD 3D H,C,C,H-TOCSY NMR experiment to measure and connect the chemical shift values of aliphatic protons of amino acid residue i, $^{1}H^{ali}_{i}$, and aliphatic carbons of amino acid residue i, $^{13}C^{ali}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$, by (i) matching the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ measured using

said RD 3D H,C,C,H-COSY NMR experiment or RD 3D H,C,C,H-TOCSY RD NMR experiment with the chemical shift values of $^{1}H^{\beta}$, $^{13}C^{\beta}$, $^{1}H^{\alpha}$, and $^{13}C^{\alpha}$ measured by said RD 3D HA,CA,(CO),N,HN NMR experiment, RD 3D HNNCAHA NMR experiment, and RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment and (ii) using the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$, to identify the type of amino acid residue *i*.

60. The method according to claim 53 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment to measure and connect the chemical shift values of a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i-1}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift value of $^{13}C'_{i-1}$ by matching the chemical shift value of $^{13}C^{\alpha}_{i}$ measured by said RD 3D HNN<CO,CA> NMR experiment with the sequentially assigned chemical shift values of $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ measured by said RD 3D HA,CA,(CO),N,HN NMR experiment and RD 3D HNNCAHA NMR experiment.

61. The method according to claim 53 further comprising:

subjecting the protein sample to (i) a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to measure and connect the chemical shift values of the β-proton of amino acid residue *i*, $^{1}H^{\beta}_{i}$, the β-carbon of amino acid residue *i*, $^{13}C^{\beta}_{i}$, the α-proton of amino acid residue *i*, $^{1}H^{\alpha}_{i}$, the α-carbon of amino acid residue *i*, $^{13}C^{\alpha}_{i}$, and a polypeptide backbone carbonyl carbon of amino acid residue *i*, $^{13}C'_{i}$ and (ii) a RD 3D HNN<CO,CA> NMR experiment to measure and connect the chemical shift values of $^{13}C'_{i}$, the α-carbon of amino acid residue *i*+1, $^{13}C^{\alpha}_{i+1}$, the polypeptide backbone amide nitrogen of amino acid residue *i*+1, $^{15}N_{i+1}$, and the polypeptide backbone amide proton of amino acid residue *i*+1, $^{1}H^{N}_{i+1}$; and

obtaining sequential assignments by matching the chemical shift value of $^{13}C'_{i}$ measured by said RD 3D HNN<CO,CA> NMR experiment with the chemical shift value of $^{13}C'_{i}$ measured by said RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment.

62. The method according to claim 53, further comprising:

subjecting the protein sample to a RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment to measure and connect the chemical shift values of aliphatic protons of amino

acid residue i-1, $^{1}H^{ali}_{i-1}$, aliphatic carbons of amino acid residue i-1, $^{13}C^{ali}_{i-1}$, $^{15}N_i$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ for amino acid residues i having unique pairs of $^{15}N_i$ and $^{1}H^{N}_{i}$ chemical shift values by matching the chemical shift values of $^{1}H^{\alpha}$ and $^{13}C^{\alpha}$ measured by said RD 3D HNNCAHA NMR experiment and RD 3D HA,CA,(CO),N,HN NMR experiment with the chemical shift values of $^{1}H^{\alpha}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and using the $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ chemical shift values to identify the type of amino acid residue i-1.

63. The method according to claim 53 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-COSY NMR experiment or a RD 3D H,C,C,H-TOCSY NMR experiment to measure and connect the chemical shift values of aliphatic protons of amino acid residue i, $^{1}H^{ali}_{i}$, and aliphatic carbons of amino acid residue i, $^{13}C^{ali}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$ by (i) matching the chemical shift values of $^{1}H^{\alpha}_{i}$ and $^{13}C^{\alpha}_{i}$ measured using said RD 3D H,C,C,H-COSY NMR experiment or RD 3D H,C,C,H-TOCSY RD NMR experiment with the chemical shift values of $^{1}H^{\alpha}$ and $^{13}C^{\alpha}$ measured by said RD 3D HA,CA,(CO),N,HN NMR experiment and RD 3D HNNCAHA NMR experiment and (ii) using the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$, to identify the type of amino acid residue i.

64. A method for sequentially assigning chemical shift values of a β-proton, $^{1}H^{\beta}$, a β-carbon, $^{13}C^{\beta}$, an α-proton, $^{1}H^{\alpha}$, an α-carbon, $^{13}C^{\alpha}$, a polypeptide backbone amide nitrogen, ^{15}N, and a polypeptide backbone amide proton, $^{1}H^{N}$, of a protein molecule comprising:

providing a protein sample;

conducting a set of reduced dimensionality (RD) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a RD three-dimensional (3D) $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment to measure and connect the chemical shift values of the β-proton of amino acid residue i-1, $^{1}H^{\beta}_{i-1}$, the β-carbon of amino acid residue i-1, $^{13}C^{\beta}_{i-1}$, the α-proton of amino acid residue i-1, $^{1}H^{\alpha}_{i-1}$, the α-carbon of amino acid residue i-1, $^{13}C^{\alpha}_{i-1}$, the polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$, and the polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$ and (2) a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR

experiment to measure and connect the chemical shift values of the β-proton of amino acid residue *i*, $^{1}H^{\beta}_{i}$, the β-carbon of amino acid residue *i*, $^{13}C^{\beta}_{i}$, the α-proton of amino acid residue *i*, $^{1}H^{\alpha}_{i}$, the α-carbon of amino acid residue *i*, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{\beta}$, $^{13}C^{\beta}$, $^{1}H^{\alpha}$, $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ by (i) matching the chemical shift values of the α- and β-protons of amino acid residue *i*-1, $^{1}H^{\alpha/\beta}_{i-1}$, and the α- and β-carbons of amino acid residue *i*-1, $^{13}C^{\alpha/\beta}_{i-1}$, with the chemical shift values of $^{1}H^{\alpha/\beta}_{i}$ and $^{13}C^{\alpha/\beta}_{i}$, (ii) using the chemical shift values of $^{1}H^{\alpha/\beta}_{i-1}$ and $^{13}C^{\alpha/\beta}_{i-1}$ to identify the type of amino acid residue *i*-1, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and using said chemical shift values to locate secondary structure elements within the polypeptide chain.

65. The method according to claim 64 further comprising:

subjecting the protein sample to a RD 3D HA,CA,(CO),N,HN NMR experiment (i) to measure and connect chemical shift values of $^{1}H^{\alpha}_{i-1}$, $^{13}C^{\alpha}_{i-1}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$ and (ii) to distinguish between NMR signals for $^{1}H^{\alpha}/^{13}C^{\alpha}$ and $^{1}H^{\beta}/^{13}C^{\beta}$ measured in said RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment and RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment.

66. The method according to claim 64 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, $^{13}C^{\alpha}_{i}$, and a polypeptide backbone carbonyl carbon of amino acid residue *i*, $^{13}C'_{i}$; and

obtaining sequential assignments of the chemical shift value of $^{13}C'_{i}$ by matching the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ measured by said RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment with the sequentially assigned chemical shift values of $^{1}H^{\beta}$, $^{13}C^{\beta}$, $^{1}H^{\alpha}$, $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ measured by said RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment and RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment.

67. The method according to claim 64 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment to measure and connect the chemical shift values of a polypeptide backbone carbonyl carbon of amino acid residue *i*-1, $^{13}C'_{i-1}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift value of $^{13}C'_{i-1}$ by matching the chemical shift value of $^{13}C^{\alpha}_{i}$ measured by said RD 3D HNN<CO,CA> NMR experiment with the sequentially assigned chemical shift values of $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ measured by said RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment and RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment.

68. The method according to claim 64 further comprising:

subjecting the protein sample to (i) a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, $^{13}C^{\alpha}_{i}$, and a polypeptide backbone carbonyl carbon of amino acid residue i, $^{13}C'_{i}$ and (ii) a RD 3D HNN<CO,CA> NMR experiment to measure and connect the chemical shift values of $^{13}C'_{i}$, the α-carbon of amino acid residue i+1, $^{13}C^{\alpha}_{i+1}$, the polypeptide backbone amide nitrogen of amino acid residue i+1, $^{15}N_{i+1}$, and the polypeptide backbone amide proton of amino acid residue i+1, $^{1}H^{N}_{i+1}$; and

obtaining sequential assignments by matching the chemical shift value of $^{13}C'_{i}$ measured by said RD 3D HNN<CO,CA> NMR experiment with the chemical shift value of $^{13}C'_{i}$ measured by said RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment.

69. The method according to claim 64 further comprising:

subjecting the protein sample to a RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment to measure and connect the chemical shift values of $^{1}H^{ali}_{i-1}$, $^{13}C^{ali}_{i-1}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ for amino acid residues i having unique pairs of $^{15}N_{i}$ and $^{1}H^{N}_{i}$ chemical shift values by matching the chemical shift values of $^{1}H^{\beta}$, $^{13}C^{\beta}$, $^{1}H^{\alpha}$, and $^{13}C^{\alpha}$ measured by said RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment and RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment with the chemical shift values of $^{1}H^{\beta}_{i-1}$, $^{13}C^{\beta}_{i-1}$, $^{1}H^{\alpha}_{i-1}$, and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and using the $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ chemical shift values to identify the type of amino acid residue i-1.

70. The method according to claim 64 further comprising:

subjecting the protein sample to a 3D HNNCACB NMR experiment to measure and connect the chemical shift value of $^{13}C^{\beta}_{i}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments by matching the chemical shift values of $^{13}C^{\beta}_{i}$ and $^{13}C^{\alpha}_{i}$ measured by said 3D HNNCACB NMR experiment with the chemical shift values of $^{13}C^{\beta}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D $\underline{H}^{\alpha/\beta}\underline{C}^{\alpha/\beta}$(CO)NHN NMR experiment.

71. The method according to claim 64 further comprising:

subjecting the protein sample to a RD two-dimensional (2D) HB,CB,(CG,CD),HD NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, and a δ-proton of amino acid residue *i* with an aromatic side chain, $^{1}H^{\delta}_{i}$; and

obtaining sequential assignments by (i) matching the chemical shift values of $^{1}H^{\beta}_{i}$ and $^{13}C^{\beta}_{i}$ measured by said RD 2D HC, CB, (CG, CD), HDNMR experiment with the chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ measured by said RD 3D $\underline{H}^{\alpha/\beta}\underline{C}^{\alpha/\beta}$(CO)NHN NMR experiment and RD 3D $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,N,HN NMR experiment, (ii) using said chemical shift values to identify amino acid residue *i* as having an aromatic side chain, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and locating amino acid residues with aromatic side chains along said polypeptide chain.

72. The method according to claim 64, further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-COSY NMR experiment or a RD 3D H,C,C,H-TOCSY NMR experiment to measure and connect the chemical shift values of aliphatic protons of amino acid residue *i*, $^{1}H^{ali}_{i}$ and aliphatic carbons of amino acid residue *i*, $^{13}C^{ali}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$ by (i) matching the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ measured using said RD 3D H,C,C,H-COSY NMR experiment or RD 3D H,C,C,H-TOCSY RD NMR experiment with the chemical shift values of $^{1}H^{\beta}$, $^{13}C^{\beta}$, $^{1}H^{\alpha}$, and $^{13}C^{\alpha}$ measured by said RD 3D $\underline{H}^{\alpha/\beta}\underline{C}^{\alpha/\beta}$(CO)NHN NMR experiment and RD 3D $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,N,HN NMR experiment, and (ii) using the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$, to identify the type of amino acid residue *i*.

73. A method for sequentially assigning the chemical shift values of aliphatic protons, $^{1}H^{ali}$, aliphatic carbons, $^{13}C^{ali}$, a polypeptide backbone amide nitrogen, ^{15}N, and a polypeptide backbone amide proton, $^{1}H^{N}$, of a protein molecule comprising:

providing a protein sample;

conducting a set of reduced dimensionality (RD) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a RD three-dimensional (3D) H,C,(C-TOCSY-CO),N,HN NMR experiment to measure and connect the chemical shift values of the aliphatic protons of amino acid residue i-1, $^{1}H^{ali}_{i-1}$, the aliphatic carbons of amino acid residue i-1, $^{13}C^{ali}_{i-1}$, the polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_i$, and the polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$ and (2) a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment to measure and connect the chemical shift values of the β-proton of amino acid residue i, $^{1}H^{\beta}_{i}$, the β-carbon of amino acid residue i, $^{13}C^{\beta}_{i}$, the α-proton of amino acid residue i, $^{1}H^{\alpha}_{i}$, the α-carbon of amino acid residue i, $^{13}C^{\alpha}_{i}$, $^{15}N_i$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}$, $^{13}C^{ali}$, ^{15}N, and $^{1}H^{N}$ by (i) matching the chemical shift values of the α- and β-protons of amino acid residue i-1, $^{1}H^{\alpha/\beta}_{i-1}$ and the α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}_{i-1}$ with the chemical shift values of $^{1}H^{\alpha/\beta}_{i}$ and $^{13}C^{\alpha/\beta}_{i}$ of amino acid residue i, (ii) using the chemical shift values of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ to identify the type of amino acid residue i-1, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and using said chemical shift values to locate secondary structure elements within the polypeptide chain.

74. The method according to claim 73 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, $^{13}C^{\alpha}_{i}$, and a polypeptide backbone carbonyl carbon of amino acid residue i, $^{13}C'_{i}$; and

obtaining sequential assignments of the chemical shift value of $^{13}C'_{i}$ by matching the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ measured by said RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment with the sequentially assigned chemical shift values of $^{1}H^{\beta}$, $^{13}C^{\beta}$, $^{1}H^{\alpha}$, $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment.

75. The method according to claim 73 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment to measure and connect the chemical shift values of a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift value of $^{13}C'_{i-1}$ by matching the chemical shift value of $^{13}C^{\alpha}_{i}$ measured by said RD 3D HNN<CO,CA> NMR experiment with the sequentially assigned chemical shift values of $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment.

76. The method according to claim 73 further comprising:

subjecting the protein sample to (i) a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, $^{13}C^{\alpha}_{i}$, and a polypeptide backbone carbonyl carbon of amino acid residue i, $^{13}C'_{i}$ and (ii) a RD 3D HNN<CO,CA> NMR experiment to measure and connect the chemical shift values of $^{13}C'_{i}$, the α-carbon of amino acid residue i+1, $^{13}C^{\alpha}_{i+1}$, the polypeptide backbone amide nitrogen of amino acid residue i+1, $^{15}N_{i+1}$, and the polypeptide backbone amide proton of amino acid residue i+1, $^{1}H^{N}_{i+1}$; and

obtaining sequential assignments by matching the chemical shift value of $^{13}C'_{i}$ measured by said RD 3D HNN<CO,CA> NMR experiment with the chemical shift value of $^{13}C'_{i}$ measured by said RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment.

77. The method according to claim 73 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment (i) to measure and connect the chemical shift values of $^{1}H^{\alpha/\beta}_{i-1}$, $^{13}C^{\alpha/\beta}_{i-1}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$, and (ii) to identify NMR signals for $^{1}H^{\alpha/\beta}_{i-1}$, $^{13}C^{\alpha/\beta}_{i-1}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$ in said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment.

78. The method according to claim 73 further comprising:

subjecting the protein sample to a RD 3D HA,CA,(CO),N,HN NMR experiment (i) to measure and connect chemical shift values of $^{1}H^{\alpha}_{i-1}$, $^{13}C^{\alpha}_{i-1}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$ and (ii) to identify NMR signals for $^{1}H^{\alpha}$ and $^{13}C^{\alpha}$ in said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment.

79. The method according to claim 73 further comprising:

subjecting the protein sample to a 3D HNNCACB NMR experiment to measure and connect the chemical shift value of $^{13}C^{\beta}_{i}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments by matching the chemical shift values of $^{13}C^{\beta}_{i}$ and $^{13}C^{\alpha}_{i}$ measured by said 3D HNNCACB NMR experiment with the chemical shift values of $^{13}C^{\beta}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment.

80. The method according to claim 73 further comprising:

subjecting the protein sample to a RD two-dimensional (2D) HB,CB,(CG,CD),HD NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, and a δ-proton of amino acid residue *i* with an aromatic side chain, $^{1}H^{\delta}_{i}$; and

obtaining sequential assignments by matching the chemical shift values of $^{1}H^{\beta}_{i}$ and $^{13}C^{\beta}_{i}$ measured by said RD 2D HB, CB, (CG, CD), HD NMR experiment with the chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ measured by said RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment and RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment, using said chemical shift values to identify amino acid residue *i* as having an aromatic side chain, and mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and locating amino acid residues with aromatic side chains along said polypeptide chain.

81. The method according to claim 73 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-COSY NMR experiment or a RD 3D H,C,C,H-TOCSY NMR experiment to measure and connect the chemical shift values of aliphatic protons of amino acid residue *i*, $^{1}H^{ali}_{i}$ and aliphatic carbons of amino acid residue *i*, $^{13}C^{ali}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$ by (i) matching the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$ measured using said RD 3D H,C,C,H-COSY NMR experiment or RD 3D H,C,C,H-TOCSY NMR experiment with the chemical shift values of $^{1}H^{ali}$ and $^{13}C^{ali}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment, and (ii) using the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$, to identify the type of amino acid residue *i*.

82. A method for sequentially assigning chemical shift values of aliphatic protons, $^{1}H^{ali}$, aliphatic carbons, $^{13}C^{ali}$, a polypeptide backbone amide nitrogen, ^{15}N, and a polypeptide backbone amide proton, $^{1}H^{N}$, of a protein molecule comprising:

providing a protein sample;

conducting a set of reduced dimensionality (RD) nuclear magnetic resonance (NMR) experiments on the protein sample comprising: (1) a RD three-dimensional (3D) H,C,(C-TOCSY-CO),N,HN NMR experiment to measure and connect the chemical shift values of the aliphatic protons of amino acid residue i-1, $^{1}H^{ali}_{i-1}$, the aliphatic carbons of amino acid residue i-1, $^{13}C^{ali}_{i-1}$, the polypeptide backbone amide nitrogen of amino acid residue i, $^{15}N_{i}$, and the polypeptide backbone amide proton of amino acid residue i, $^{1}H^{N}_{i}$ and (2) a RD 3D HNNCAHA NMR experiment to measure and connect the chemical shift values of the α-proton of amino acid residue i, $^{1}H^{\alpha}_{i}$, the α-carbon of amino acid residue i, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}$, $^{13}C^{ali}$, ^{15}N, and $^{1}H^{N}$ by (i) matching the chemical shift values of the α-proton of amino acid residue i-1, $^{1}H^{\alpha}_{i-1}$, and the α-carbon of amino acid residue i-1, $^{13}C^{\alpha}_{i-1}$, with the chemical shift values of $^{1}H^{\alpha}_{i}$ and $^{13}C^{\alpha}_{i}$, (ii) using the chemical shift values of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ to identify the type of amino acid residue i-1, and (iii) mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and using said chemical shift values to locate secondary structure elements within the polypeptide chain.

83. The method according to claim 82 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to measure and connect the chemical shift values of a β-proton of amino acid residue i, $^{1}H^{\beta}_{i}$, a β-carbon of amino acid residue i, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, $^{13}C^{\alpha}_{i}$, and a polypeptide backbone carbonyl carbon of amino acid residue i, $^{13}C'_{i}$; and

obtaining sequential assignments of the chemical shift value of $^{13}C'_{i}$ by matching the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ measured by said RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment with the sequentially assigned chemical shift values of $^{1}H^{\beta}$, $^{13}C^{\beta}$, $^{1}H^{\alpha}$, $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and RD 3D HNNCAHA NMR experiment.

84. The method according to claim 82 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment to measure and connect the chemical shift values of a polypeptide backbone carbonyl carbon of amino acid residue i-1, $^{13}C'_{i-1}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments of the chemical shift value of $^{13}C'_{i-1}$ by matching the chemical shift value of $^{13}C^{\alpha}_{i}$ measured by said RD 3D HNN<CO,CA> NMR experiment with the sequentially assigned chemical shift values of $^{13}C^{\alpha}$, ^{15}N, and $^{1}H^{N}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and RD 3D HNNCAHA NMR experiment.

85. The method according to claim 82 further comprising:

subjecting the protein sample to (i) a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to measure and connect the chemical shift values of a β-proton of amino acid residue i, $^{1}H^{\beta}_{i}$, a β-carbon of amino acid residue i, $^{13}C^{\beta}_{i}$, the α-proton of amino acid residue i, $^{1}H^{\alpha}_{i}$, the α-carbon of amino acid residue i, $^{13}C^{\alpha}_{i}$, and a polypeptide backbone carbonyl carbon of amino acid residue i, $^{13}C'_{i}$ and (ii) a RD 3D HNN<CO,CA> NMR experiment to measure and connect the chemical shift values of $^{13}C'_{i}$, an α-carbon of amino acid residue i+1, $^{13}C^{\alpha}_{i+1}$, a polypeptide backbone amide nitrogen of amino acid residue i+1, $^{15}N_{i+1}$, and a polypeptide backbone amide proton of amino acid residue i+1, $^{1}H^{N}_{i+1}$; and

obtaining sequential assignments by matching the chemical shift value of $^{13}C'_{i}$ measured by said RD 3D HNN<CO,CA> NMR experiment with the chemical shift value of $^{13}C'_{i}$ measured by said RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment.

86. The method according to claim 82 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment (i) to measure and connect the chemical shift values of the α- and β-protons of amino acid residue i-1, $^{1}H^{\alpha/\beta}_{i-1}$, α- and β-carbons of amino acid residue i-1, $^{13}C^{\alpha/\beta}_{i-1}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$, and (ii) to distinguish NMR signals for the chemical shift values of $^{1}H^{\beta}_{i-1}$, $^{13}C^{\beta}_{i-1}$, $^{1}H^{\alpha}_{i-1}$, and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment from NMR signals for the chemical shift values of $^{1}H^{ali}_{i-1}$ and $^{13}C^{ali}_{i-1}$ other than $^{1}H^{\alpha/\beta}_{i-1}$ and $^{13}C^{\alpha/\beta}_{i-1}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment.

87. The method according to claim 82 further comprising:

subjecting the protein sample to a RD 3D $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,N,HN NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments by matching the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ measured by said RD 3D $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,N,HN NMR experiment with the chemical shift values of $^{1}H^{\beta}_{i-1}$, $^{13}C^{\beta}_{i-1}$, $^{1}H^{\alpha}_{i-1}$, and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D $\underline{H}$,$\underline{C}$,(C-TOCSY-CO),N,HN NMR experiment.

88. The method according to claim 82 further comprising:

subjecting the protein sample to a 3D HNNCACB NMR experiment to measure and connect the chemical shift values of $^{13}C^{\beta}_{i}$, $^{13}C^{\alpha}_{i}$, $^{15}N_{i}$, and $^{1}H^{N}_{i}$; and

obtaining sequential assignments by matching the chemical shift values of $^{13}C^{\beta}_{i}$ and $^{13}C^{\alpha}_{i}$ measured by said 3D HNNCACB NMR experiment with the chemical shift values of $^{13}C^{\beta}_{i-1}$ and $^{13}C^{\alpha}_{i-1}$ measured by said RD 3D $\underline{H}$,$\underline{C}$,(C-TOCSY-CO),N,HN NMR experiment.

89. The method according to claim 82 further comprising:

subjecting the protein sample to a RD two-dimensional (2D) $\underline{HB}$,$\underline{CB}$,(CG,CD),HD NMR experiment to measure and connect the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, and a δ-proton of amino acid residue *i* with an aromatic side chain, $^{1}H^{\delta}_{i}$; and

obtaining sequential assignments by matching the chemical shift values of $^{1}H^{\beta}_{i}$ and $^{13}C^{\beta}_{i}$ measured by said RD 2D $\underline{HB}$, $\underline{CB}$,(CG, CD), HD NMR experiment with the chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$ measured by said RD 3D $\underline{H}$,$\underline{C}$,(C-TOCSY-CO),N,HN NMR experiment, using said chemical shift values to identify amino acid residue *i* as having an aromatic side chain, and mapping sets of sequentially connected chemical shift values to the amino acid sequence of the polypeptide chain and locating amino acid residues with aromatic side chains along said polypeptide chain.

90. The method according to claim 82 further comprising:

subjecting the protein sample to a RD 3D $\underline{H}$,$\underline{C}$,C,H-COSY NMR experiment or a RD 3D $\underline{H}$,$\underline{C}$,C,H-TOCSY NMR experiment to measure and connect the chemical shift values of aliphatic protons of amino acid residue *i*, $^{1}H^{ali}_{i}$ and aliphatic carbons of amino acid residue *i*, $^{13}C^{ali}_{i}$; and

obtaining sequential assignments of the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$ by (i) matching the chemical shift values of $^{1}H^{ali}$ and $^{13}C^{ali}$ measured using said RD 3D H,C,C,H-COSY NMR experiment or RD 3D H,C,C,H-TOCSY NMR experiment with the chemical shift values of $^{1}H^{\beta}_{i}$, $^{13}C^{\beta}_{i}$, $^{1}H^{\alpha}_{i}$, and $^{13}C^{\alpha}_{i}$ measured by said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and RD 3D HNNCAHA NMR experiment, and (ii) using the chemical shift values of $^{1}H^{ali}_{i}$ and $^{13}C^{ali}_{i}$, to identify the type of amino acid residue *i*.

91. A method for obtaining assignments of chemical shift values of ^{1}H, ^{13}C and ^{15}N of a protein molecule comprising:

providing a protein sample; and

conducting four reduced dimensionality (RD) nuclear magnetic resonance (NMR) experiments on the protein sample, wherein (1) a first experiment is selected from the group consisting of a RD three-dimensional (3D) $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment, a RD 3D HA,CA,(CO),N,HN NMR experiment, and a RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment for obtaining sequential correlations of chemical shift values; (2) a second experiment is selected from the group consisting of a RD 3D HNNCAHA NMR experiment, a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment, and a RD 3D HNN<CO,CA> NMR experiment for obtaining intraresidue correlations of chemical shift values; (3) a third experiment is a RD 3D H,C,C,H-COSY NMR experiment for obtaining assignments of sidechain chemical shift values; and (4) a fourth experiment is a RD two-dimensional (2D) HB,CB,(CG,CD),HD NMR experiment for obtaining assignments of aromatic sidechain chemical shift values.

92. The method according to claim 91 further comprising:

subjecting the protein sample to a RD 2D H,C,H-COSY NMR experiment for obtaining assignments of sidechain chemical shift values.

93. The method according to claim 91, wherein the first experiment is the RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment and the second experiment is the RD 3D HNNCAHA NMR experiment.

94. The method according to claim 93 further comprising:

subjecting the protein sample to a RD 3D HA,CA,(CO),N,HN NMR experiment to distinguish between NMR signals for $^{1}H^{\alpha}/^{13}C^{\alpha}$ and $^{1}H^{\beta}/^{13}C^{\beta}$ from said RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment.

95. The method according to claim 93 further comprising:

subjecting the protein sample to a RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment to obtain assignments of chemical shift values of $^{1}H^{ali}$ and $^{13}C^{ali}$.

96. The method according to claim 93 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment to obtain assignments of chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$.

97. The method according to claim 93 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment to obtain assignments of chemical shift values of polypeptide backbone carbonyl carbons, $^{13}C'$.

98. The method according to claim 93 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to obtain assignments of chemical shift values of polypeptide backbone carbonyl carbons, $^{13}C'$.

99. The method according to claim 93 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment and a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to obtain assignments of chemical shift values of $^{13}C'$.

100. The method according to claim 93 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-TOCSY NMR experiment to obtain assignments of chemical shift values of ^{1}H and ^{13}C of aliphatic sidechains.

101. The method according to claim 93 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-TOCSY NMR experiment to obtain assignments of chemical shift values of ^{1}H and ^{13}C of aromatic sidechains.

102. The method according to claim 93 further comprising:

subjecting the protein sample to a 3D HNNCACB NMR experiment to obtain assignments of chemical shift values of $^{13}C^{\beta}$.

103. The method according to claim 93, wherein the first experiment is the RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and the second experiment is the RD 3D HNNCAHA NMR experiment.

104. The method according to claim 103 further comprising:

subjecting the protein sample to a RD 3D HA,CA,(CO),N,HN NMR experiment to identify NMR signals for $^{1}H^{\alpha}/^{13}C^{\alpha}$ in said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment.

105. The method according to claim 103 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment to obtain assignments of chemical shift values of $^{1}H^{\beta}$ and $^{13}C^{\beta}$.

106. The method according to claim 103 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment to obtain assignments of chemical shift values of polypeptide backbone carbonyl carbons, $^{13}C'$.

107. The method according to claim 103 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to obtain assignments of chemical shift values of polypeptide backbone carbonyl carbons, $^{13}C'$.

108. The method according to claim 103 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment and a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to obtain assignments of chemical shift values of $^{13}C'$.

109. The method according to claim 103 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-TOCSY NMR experiment to obtain assignments of chemical shift values of ^{1}H and ^{13}C of aliphatic sidechains.

110. The method according to claim 103 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-TOCSY NMR experiment to obtain assignments of chemical shift values of ^{1}H and ^{13}C of aromatic sidechains.

111. The method according to claim 103 further comprising:

subjecting the protein sample to a 3D HNNCACB NMR experiment to obtain assignments of chemical shift values of $^{13}C^{\beta}$.

112. The method according to claim 91, wherein the first experiment is the RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and the second experiment is the RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,N,HN NMR experiment.

113. The method according to claim 112 further comprising:

subjecting the protein sample to a RD 3D HA,CA,(CO),N,HN NMR experiment to identify NMR signals for $^{1}H^{\alpha}$ and $^{13}C^{\alpha}$ in said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment.

114. The method according to claim 112 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment to identify NMR signals for $^{1}H^{\alpha/\beta}$ and $^{13}C^{\alpha/\beta}$ in said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment.

115. The method according to claim 112 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment to obtain assignments of chemical shift values of polypeptide backbone carbonyl carbons, $^{13}C'$.

116. The method according to claim 112 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to obtain assignments of chemical shift values of polypeptide backbone carbonyl carbons, $^{13}C'$.

117. The method according to claim 112 further comprising:

subjecting the protein sample to a RD 3D HNN<CO,CA> NMR experiment and a RD 3D $H^{\alpha/\beta}$,$C^{\alpha/\beta}$,CO,HA NMR experiment to obtain assignments of chemical shift values of $^{13}C'$.

118. The method according to claim 112 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-TOCSY NMR experiment to obtain assignments of chemical shift values of ^{1}H and ^{13}C of aliphatic sidechains.

119. The method according to claim 112 further comprising:

subjecting the protein sample to a RD 3D H,C,C,H-TOCSY NMR experiment to obtain assignments of chemical shift values of ^{1}H and ^{13}C of aromatic sidechains.

120. The method according to claim 112 further comprising:

subjecting the protein sample to a 3D HNNCACB NMR experiment to obtain assignments of chemical shift values of $^{13}C^{\beta}$.

121. The method according to claim 91, wherein the first experiment is the RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment and the second experiment is the RD 3D HNN<CO,CA> NMR experiment.

122. The method according to claim 121 further comprising:

subjecting the protein sample to a RD 3D HA,CA,(CO),N,HN NMR experiment to identify NMR signals for $^{1}H^{\alpha}$ and $^{13}C^{\alpha}$ in said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment.

123. The method according to claim 121 further comprising:

subjecting the protein sample to a RD 3D $H^{\alpha/\beta}C^{\alpha/\beta}$(CO)NHN NMR experiment to identify NMR signals for $^{1}H^{\alpha/\beta}$ and $^{13}C^{\alpha/\beta}$ in said RD 3D H,C,(C-TOCSY-CO),N,HN NMR experiment.

124. The method according to claim 121 further comprising:

subjecting the protein sample to a RD 3D $\underline{H}^{\alpha/\beta}$,$\underline{C}^{\alpha/\beta}$,CO,HA NMR experiment to obtain assignments of chemical shift values of polypeptide backbone carbonyl carbons, $^{13}C'$.

125. The method according to claim 121 further comprising:

subjecting the protein sample to a RD 3D $\underline{H}$,$\underline{C}$,C,H-TOCSY NMR experiment to obtain assignments of chemical shift values of ^{1}H and ^{13}C of aliphatic sidechains.

126. The method according to claim 121 further comprising:

subjecting the protein sample to a RD 3D $\underline{H}$,$\underline{C}$,C,H-TOCSY NMR experiment to obtain assignments of chemical shift values of ^{1}H and ^{13}C of aromatic sidechains.

127. The method according to claim 121 further comprising:

subjecting the protein sample to a 3D HNNCACB NMR experiment to obtain assignments of chemical shift values of $^{13}C^{\beta}$.

128. The method according to claim 91 further comprising:

subjecting the protein sample to nuclear Overhauser effect spectroscopy (NOESY) to deduce the tertiary structure of the protein molecule.

129. The method according to claim 91 further comprising:

subjecting the protein sample to NMR experiments that measure scalar coupling constants to deduce the tertiary structure of the protein molecule.

130. The method according to claim 91 further comprising:

subjecting the protein sample to NMR experiments that measure residual dipolar coupling constants to deduce the tertiary structure of the protein molecule.